Gigsaw Next Gen Sequence Assembly Simulator

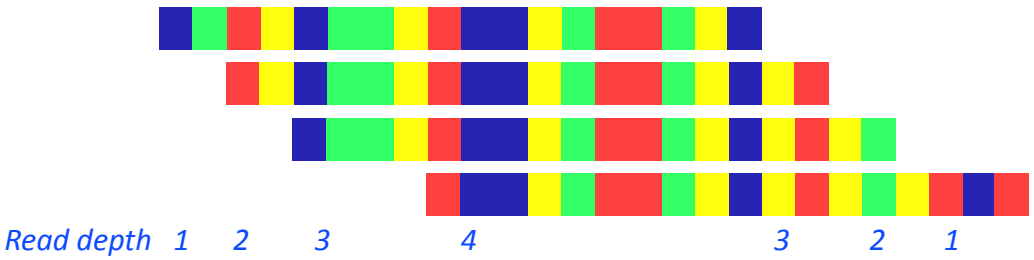
Print out the sequence reads and reference sequence sheets.
Make sure that *reads sheet 1 forward* is on the back of the same sheet of paper as *reads sheet 1 reverse* and ensure that the reads align.

Cut out the reads along the white horizontal gaps.

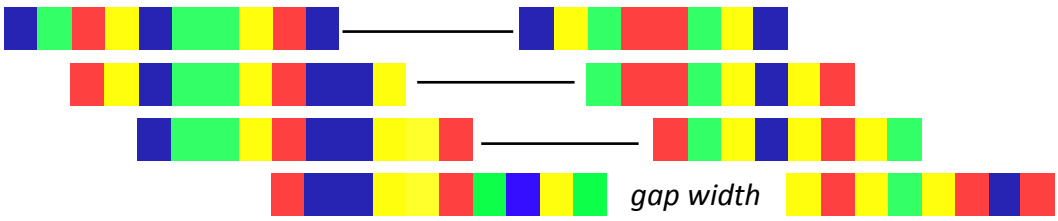
For paired end reads, carefully divide them as shown in the figure below

The reference sequence can be assembled by using the grey box on the row end as a tab on which to stick the previous sequence portion (positions are numbered above the sequence).

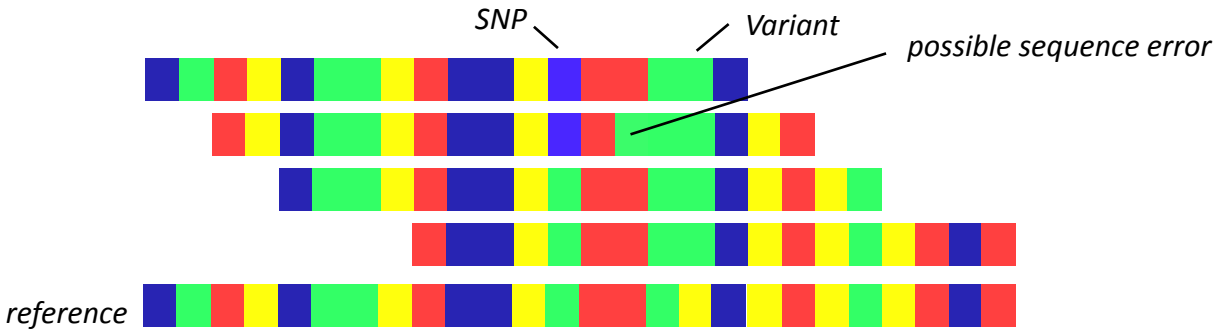
For a normal assembly, try to overlap the reads as much as possible. You should end up with approximately the read depth of reads at all points in the final assembly. Remember that the reverse complement sequence (the other strand of DNA) can be found on the reverse side.



For paired end reads, place them facing each other approximately the gap size apart. Again attempt to align them as well as you can.



For aligning against the reference sequence, try to find the position where the sequence best matches. If you are looking for SNPs or have a high error rate then there may not be a perfect match.

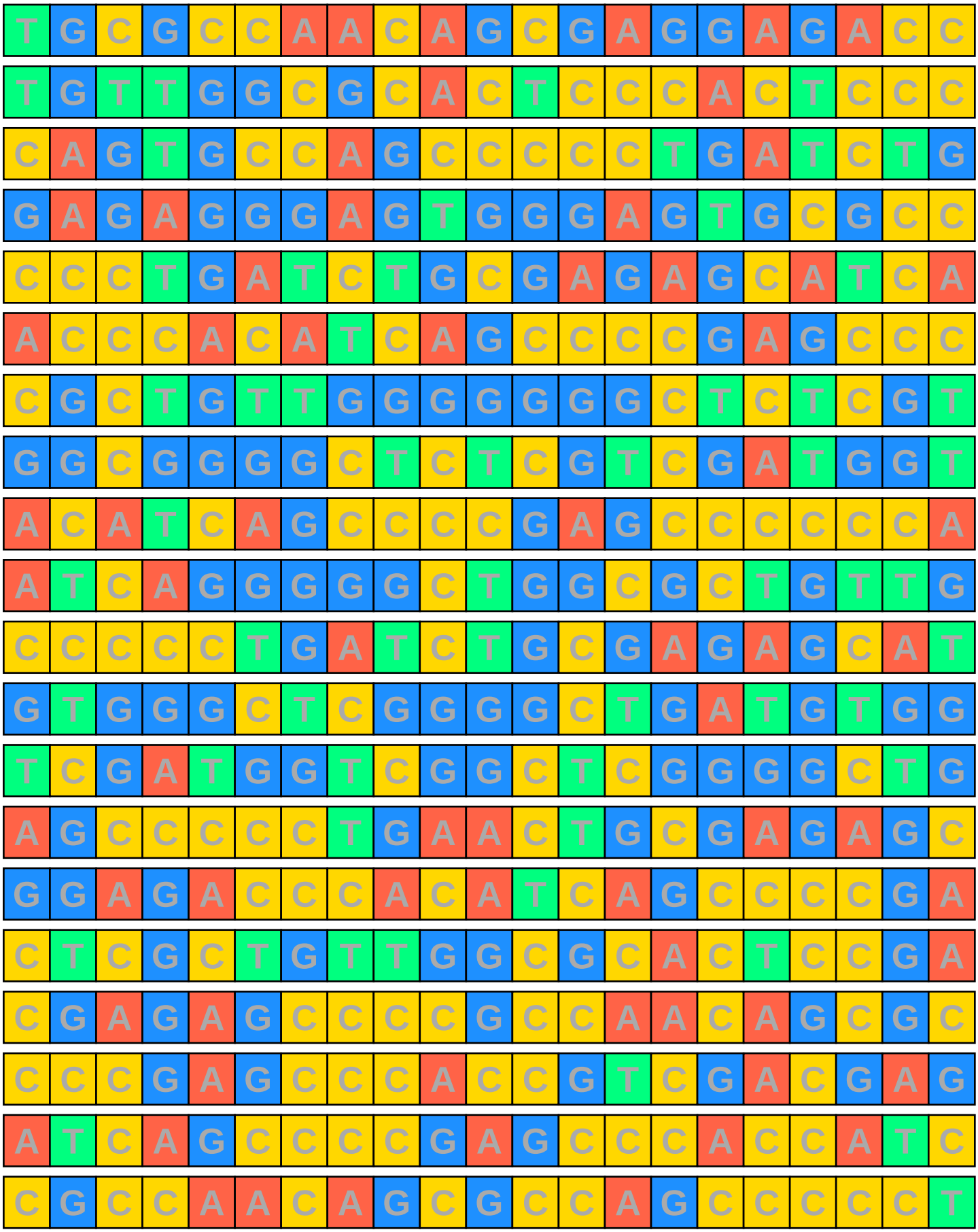


Gigsaw created by Dr David Martin, University of Dundee, Scotland

Gigsaw Parameters for RNAseq reads

Sequence Length	**117**
Coverage	**7.2**
Error rate	**15/1000 bases**
Polymorphisms	**Sequence contains 0 polymorphisms**

RNAseq reads sheet 1 forward reads



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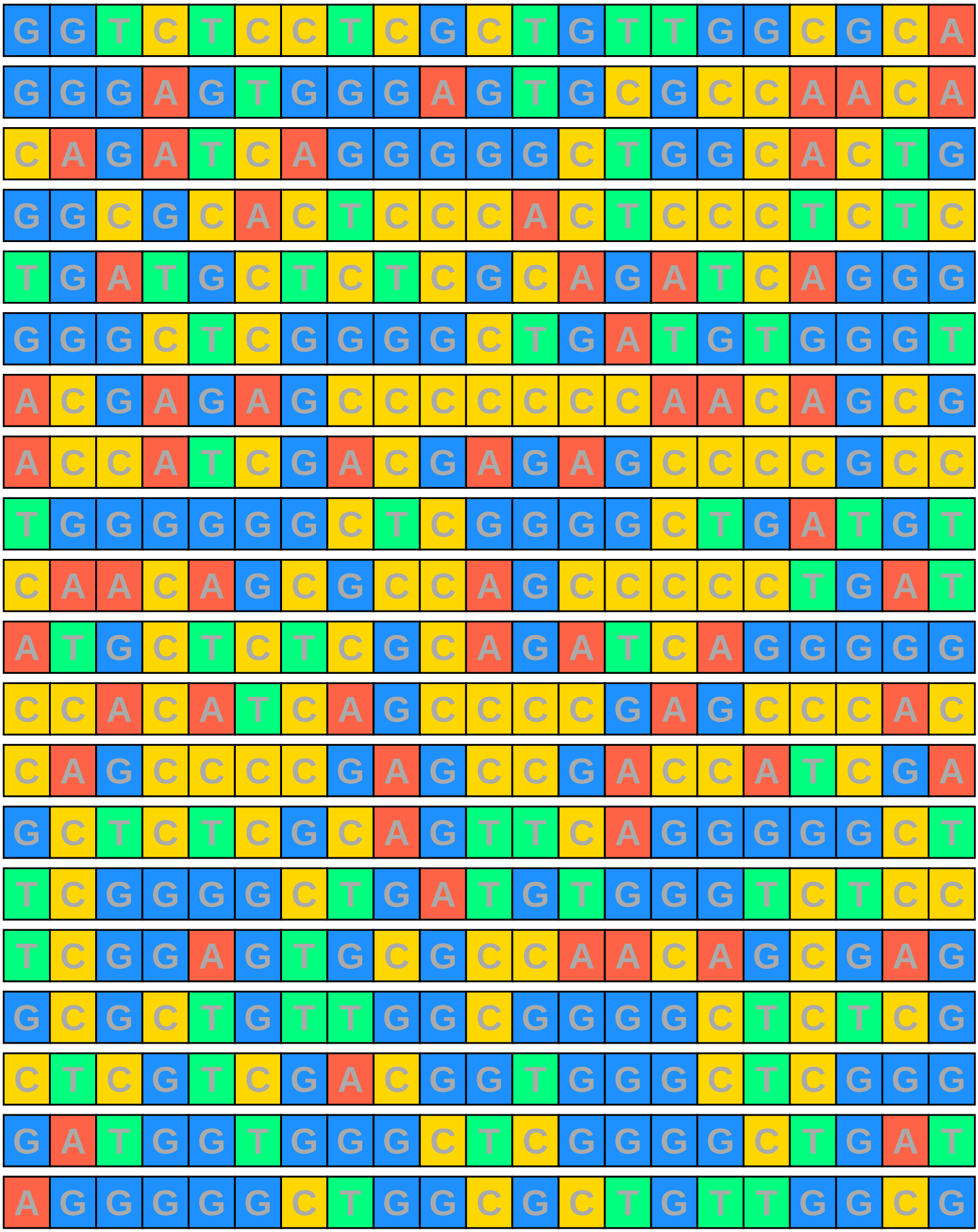
RNAseq reads sheet 1 reverse reads



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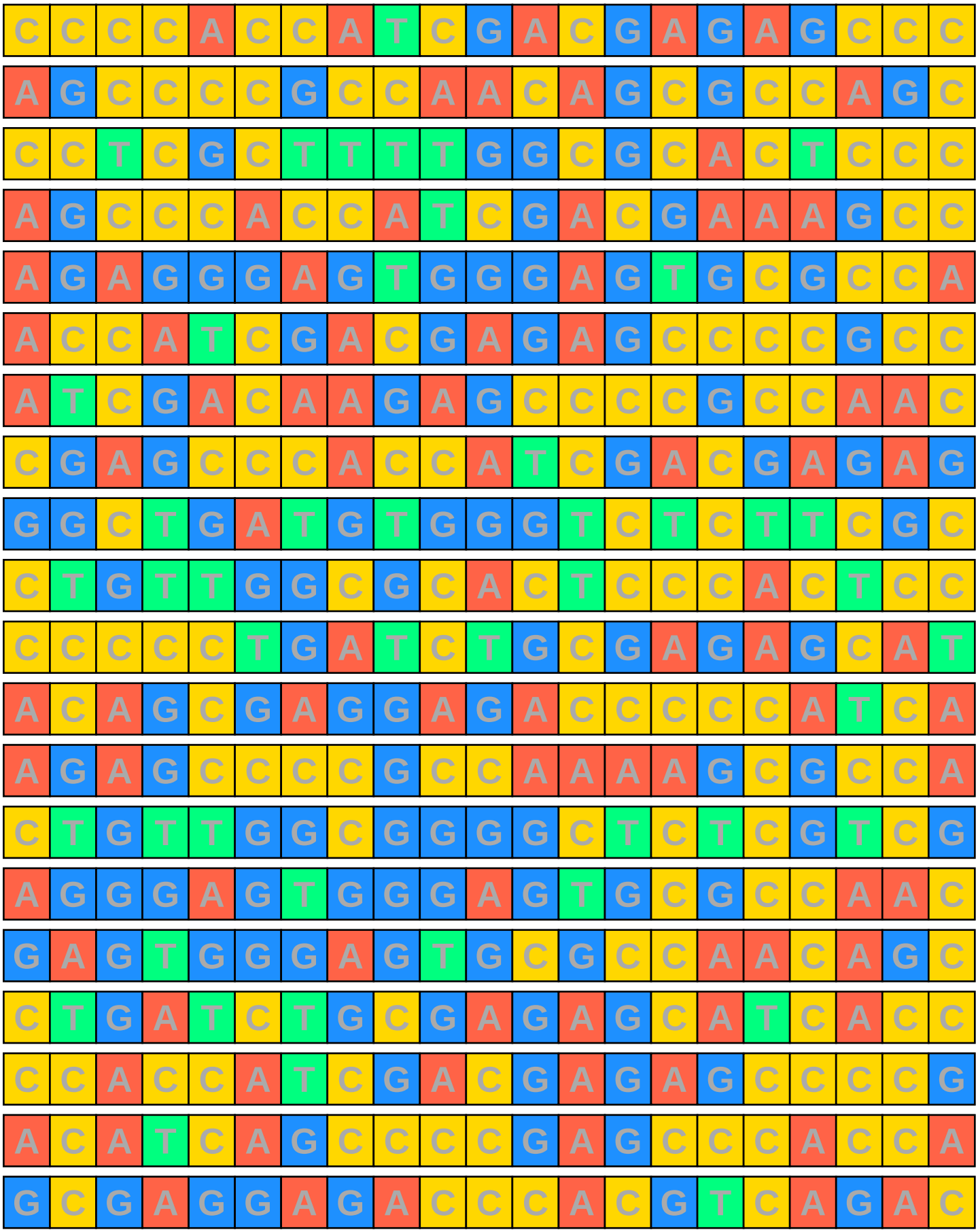
RNAseq reads sheet 2 forward reads



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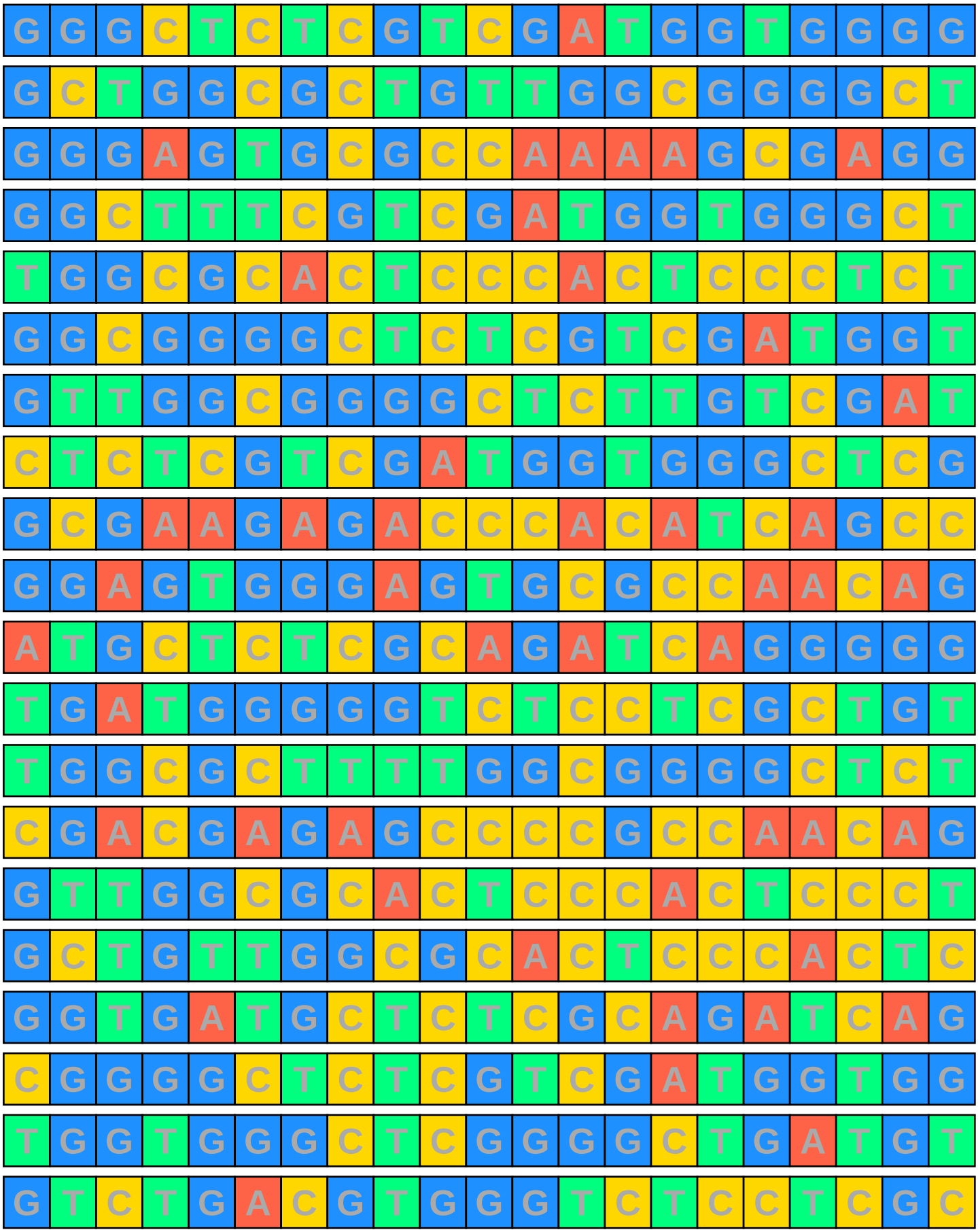
RNAseq reads sheet 2 reverse reads



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